

REMARKS

It is believed that by submitting the present amendment the application now fully complies with the requirements of 37 CFR 1.821-1.825. Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11.0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

KEIL & WEINKAUF

A handwritten signature in black ink, appearing to read "Daniel S. Kim", written in a cursive style.

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**VERSION WITH MARKINGS TO SHOW CHANGES MADE**

Amend the paragraph on page 4, lines 1-3, as follows:

The instant invention pertains further to an enzyme comprising an amino acid sequence as set forth in SEQ ID NO. [1a, 2b or 5a] 16, 22 or 20 or a functional fragment, derivative, allele, homologue or isoenzyme thereof.

Amend the paragraph on page 4, lines 13-27, as follows:

Also, partially sequenced cDNA clone from *Neurospora crassa* (SEQ ID NO. 9) and a *Zea mays* EST (Extended Sequence Tac) clone (SEQ ID NO. 7) and corresponding putative amino acid sequence (SEQ ID NO. 8) were identified. Finally, two cDNA clones were identified, one *Arabidopsis thaliana* EST (SEQ ID NO. 5 and corresponding predicted amino acid sequence SEQ ID NO. 6) and a *Lycopersicon esculentum* EST clone (SEQ ID NO. 12) were identified. Further, enzymes designated as PDAT comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. [2a, 3a, 5b, 6 or 7b] 17, 18, 25, 6 or 27 are contemplated within the scope of the invention. Moreover, an enzyme comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivative, allele or homologue thereof selected from the group consisting of sequences as set forth in SEQ ID NO. [1, 1b, 3, 3b, 4, 4a, 4b, 5, 5b, 6b, 7, 8b, 9, 9b, 10, 10b, 11, 11b or 12] 21, 3, 23, 4, 19, 24, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31 or 12 or a functional fragment, derivative, allele, homologue or isoenzyme of the enzyme encoding amino acid sequence are included within the scope of the invention.

Amend the paragraph on page 7, lines 1-11, as follows:

Further included is a nucleotide sequence selected from the group consisting of sequences set forth in SEQ ID NO. [1, 1b, 3, 3b, 4, 4a, 4b, 9b, 10, 10b or 11] 21, 3, 23, 4, 19, 26, 29, 10, 30 or 11 or a portion, derivative, allele or homologue thereof. The invention pertains a partial nucleotide sequence corresponding to a fulllength nucleotide sequence selected from the group consisting of sequences set forth in SEQ ID NO. [5, 5b, 6b, 7, 8b, 9, 11b or 12] 5, 25, 26, 7, 28, 9, 31 or 12 or a portion, derivative, allele or homologue thereof. Moreover, a nucleotide sequence comprising a nucleotide sequence which is at least 40% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in SEQ ID NO. [1, 1b, 3, 3b, 4, 4a, 4b, 5, 5b, 6b, 7, 8b, 9, 9b, 10, 10b, 11, 11b or 12] 1, 21, 3, 23, 4, 19, 24, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31 or 12 is contemplated within the scope of the invention.

Amend the paragraph on page 21, lines 17-26, as follows:

PDAT genes. Nucleotide and amino acid sequences of several PDAT genes are given as SEQ ID NO. 1 through 15. Further provisional and/or partial sequences are given as SEQ ID NO. [1a through 5a and 1b through 11b] 16 through 20 and 21 through 31, respectively. One of the Arabidopsis genomic sequences (SEQ ID NO. 4) identified an Arabidopsis EST cDNA clone; T04806. This cDNA clone was fully characterized and the nucleotide sequence is given as SEQ ID NO. 5. Based on the sequence homology of the T04806 cDNA and the *Arabidopsis thaliana* genomic DNA sequence (SEQ ID NO. 4) it is apparent that an additional A is present at position 417 in the cDNA clone (data not shown). Excluding this nucleotide would give the amino

acid sequence depicted in SEQ ID NO. 12.

Amend the paragraphs from page 35, line 25 through page 37, line 15, as follows:

SEQ ID NO. [1a] 16: The amino acid sequence of the yeast ORF YNR008w from *Saccharomyces cerevisiae*.

SEQ ID NO. [2a] 17: Amino acid sequence of the region of the *Arabidopsis thaliana* genomic sequence (AC004557).

SEQ ID NO. [3a] 18: Amino acid sequence of the region of the *Arabidopsis thaliana* genomic sequence (AB006704).

SEQ ID NO. [4a] 19: The corresponding genomic DNA sequence and amino acid sequence of the yeast ORF YNROO8w from *Saccharomyces cerevisiae*.

SEQ ID NO. [5a] 20: The amino acid sequence of the yeast ORF YNROO8w from *Saccharomyces cerevisiae* derived from the corresponding genomic DNA sequence.

SEQ ID NO. [1b] 21: Genomic DNA sequence of the *Saccharomyces cerevisiae* PDAT gene, YNR008w, genebank nucleotide ID number 1302481, and the suggested YNR008w amino acid sequence.

SEQ ID NO. [2b] 22: The suggested amino acid sequence of the yeast gene YNR008w from *Saccharomyces cerevisiae*.

SEQ ID NO. [3b] 23: Genomic DNA sequence of the *Schizosaccharomyces pombe* gene SPBC776.14.

SEQ ID NO. [4b] 24: Genomic DNA sequence of a part of the *Arabidopsis thaliana*

locus with genebank accession number AB006704.

SEQ ID NO. [5b] 25: Nucleotide sequence and the corresponding amino acid sequence of the *Arabidopsis thaliana* EST-clone with genebank accession number T04806, and ID number 315966.

SEQ ID NO. [6b] 26: Nucleotide and amino acid sequence of the *Zea mays* cDNA clone with genebank ID number g4388167.

### **IN THE CLAIMS**

Amend claims 4-6 and 9-11 as follows:

4. (twice amended) An enzyme according to claim 1, comprising an amino acid sequence as set forth in SEQ ID NO. [1a, 2b or 5a] 16, 22 or 20 or a functional fragment, derivative, allele, homologue or isoenzyme thereof.

5. (twice amended) An enzyme according to claim 1, comprising an amino acid sequence selected from the group consisting of sequences as set forth in SEQ ID NO. [2a, 3a, 5b, 6, 7b,] 17, 18, 25, 6, 27, 8, 13, 14, 15 or a functional fragment, derivative, allele, homologue or isoenzyme thereof.

6. (twice amended) An enzyme according to claim 1, comprising an amino acid sequence encoded through a nucleotide sequence, a portion, derivative, allele or homologue thereof selected from the group consisting of sequences as set forth in SEQ ID NO. [1, 1b, 3, 3b, 4, 4a, 4b, 5, 5b, 6b, 7, 8b, 9, 9b, 10, 10b, 11, 11b, 12] 1, 21, 3, 23, 4, 19, 26, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31, 12, or a functional fragment, derivative, allele, homologue or isoenzyme of the enzyme encoding amino acid sequence.

9. (twice amended) A nucleotide sequence according to claim 7, selected from

the group consisting of sequences as set forth in SEQ ID NO. [1, 1b, 3, 3b, 4, 4a, 4b, 9b, 10, 10b or 11] 1, 21, 3, 23, 4, 19, 24, 29, 10, 30 or 11 or a portion, derivative, allele or homologue thereof.

10. (amended) A partial nucleotide sequence corresponding to a fulllength nucleotide sequence according to claim 7, selected from the group consisting of sequences as set forth in SEQ ID NO. [5, 5b, 6b, 7, 8b, 9, 11b or 12] 5, 25, 26, 7, 28, 9, 31 or 12 or a portion, derivative, allele or homologue thereof.

11. (amended) A nucleotide sequence according to claim 7, comprising a nucleotide sequence which is at least 40% homologous to a nucleotide sequence selected from the group consisting of those sequences as set forth in SEQ ID NO. [1, 1b, 3, 3b, 4, 4a, 4b, 5, 5b, 6b, 7, 8b, 9, 10, 10b, 11, 11b or 12] 1, 21, 3, 23, 4, 19, 24, 5, 25, 26, 7, 28, 9, 29, 10, 30, 11, 31 or 12.

SEQ ID NO. [7b] 27:

SEQ ID NO. [8b] 28:

SEQ ID NO. [9b] 29:

SEQ ID NO. [10b] 30:

SEQ ID NO. [11b] 31: